

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(I) APPLICANT:

- (A) NAME: LUDWIG INSTITUTE FOR CANCER RESEARCH
- (B) STREET: 1345 AVENUE OF THE AMERICAS
- (C) CITY: NEW YORK
- (D) STATE: NEW YORK
- (E) COUNTRY: UNITED STATES OF AMERICA
- (F) POSTAL CODE: 10105

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(I) APPLICANT/INVENTOR:

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- (A) NAME: LETHÉ, BERNARD
- (B) STREET: AVENUE HIPPOCRATE 74, UCL 7459
- (C) CITY: BRUSSELS
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE: 1200

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(i) APPLICANT/INVENTOR:

- (A) NAME: LUCAS, SOPHIE
- (B) STREET: AVENUE HIPPOCRATE 74, UCL 7459
- (C) CITY: BRUSSELS
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE: 1200

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(i) APPLICANT/INVENTOR:

- (A) NAME: DE SMET, CHARLES
- (B) STREET: AVENUE HIPPOCRATE 74, UCL 7459
- (C) CITY: BRUSSELS
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE: 1200

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(i) APPLICANT/INVENTOR:

- (A) NAME: GODELAINE, DANIELE
- (B) STREET: AVENUE HIPPOCRATE 74, UCL 7459
- (C) CITY: BRUSSELS
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE: 1200

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(i) APPLICANT/INVENTOR:

- (A) NAME: BOON-FALLEUR, THIERRY
- (B) STREET: AVENUE HIPPOCRATE 74, UCL 7459
- (C) CITY: BRUSSELS
- (E) COUNTRY: BELGIUM
- (F) POSTAL CODE: 1200

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(ii) TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS

(iii) NUMBER OF SEQUENCES: 14

5 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.

(B) STREET: 600 ATLANTIC AVENUE

(C) CITY: BOSTON

(D) STATE: MASSACHUSETTS

10 (E) COUNTRY: UNITED STATES OF AMERICA

(F) POSTAL CODE: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

15 (B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

20 (A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: 08/791,495

(B) FILING DATE: 27-JAN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Van Amsterdam, John R.

30 (B) REGISTRATION NUMBER: 40,212

(C) REFERENCE/DOCKET NUMBER: L0461/7005WO

(ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 617-720-3500

(B) TELEFAX: 617-720-2441

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10 GATCTCAGAA CACCCAAACA CAAGGTCTCA GAACAGAGAC CTGGTACACC AGGCCCGCCG 60
CCACCCGAGG GAGCCCAGGG AGATGGGTGC AGAGGTGTCG CCTTTAATGT GATGTTCTCT 120
GCCCCTCACA TTTAGCCGAC TGA CTGCTGC AGACCACCGC CAACTGCAGC TCTCCATCAG 180
15 CTCCTGTCTC CAGCAGCTTT CCCTGTTGAT GTGGATC 217

(2) INFORMATION FOR SEQ ID NO:2:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATGGGTGC AGAGGTGT 18

(2) INFORMATION FOR SEQ ID NO:3:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10 GATCCACATC AACAGGGAA

19

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1002 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

30

(A) NAME/KEY: CDS

(B) LOCATION: 65..697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35 TCTGCCTCCG CATCCTCGTG GGCCCTGACC TTCTCTCTGA GAGCCGGGCA GAGGCTCCGG 60

AGCC ATG CAG GCC GAA GGC CAG GGC ACA GGG GGT TCG ACG GGC GAT GCT 109

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala

1

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GAT GGC CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT 157

Asp Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala

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30

45 GGC GGC CCA GGA GAG GCG GST GCC ACG GGC GGC AGA GGT CCC CGG GGC 205

Gly Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly

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	GCA GGG GCA GCA AGG GCC TCG GGG CCG AGA GGA GGC GCC CCG CGG GGT	253
	Ala Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly	
	50 55 60	
5	CCG CAT GGC GGT GCC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG	301
	Pro His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly	
	65 70 75	
	GCC AGG AGG CCG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG CCT	349
10	Ala Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro	
	80 85 90 95	
	TTC TCG TCG CCC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG	397
15	Phe Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg	
	100 105 110	
	GAT GCC GCA CCT CTC CCC CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC	445
20	Asp Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr	
	115 120 125	
	GTG TCC GGC AAC CTA CTG TTT ATG TCA GTT CGG GAC CAG GAC AGG GAA	493
	Val Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu	
	130 135 140	
25	GGC GCT GGG CGG ATG AGG GTG GTG GGT TGG GGG CTG GGA TCC GCC TCC	541
	Gly Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser	
	145 150 155	
	CCG GAG GGG CAG AAA GCT AGA GAT CTC AGA ACA CCC AAA CAC AAG GTC	589
30	Pro Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val	
	160 165 170 175	
	TCA GAA CAG AGA CCT GGT ACA CCA GGC CCG CCG CCA CCC GAG GGA GCC	637
35	Ser Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala	
	180 185 190	
	CAG GGA GAT GGG TGC AGA GGT GTC GCC TTT AAT GTG ATG TTC TCT GCC	685
40	Gln Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala	
	195 200 205	
	CCT CAC ATT TAGCCGACTG ACTGCTGCAG ACCACCGCCA ACTGCAGCTC	734
	Pro His Ile	
	210	
45	TCCATCAGCT CCTGTCTCCA GCAGCTTTCC CTGTTGATGT GGATCAGCA GTGCTTTCTG	794
	CCCGTGTTTT TGGCTCAGGC TCCCTCAGGG CAGAGGCGCT AAGCCCAGCC TGSCGCCCT	854

TCCTAGGTCA TGCCTCCTCC CCTAGGGAAT GGTCCCAGCA CGAGTGGCCA GTTCATTGTG 914

GGGGCCTGAT TGTITGTCGC TGGAGGAGGA CGGCTTACAT GTTTGTTTCT GTAGAAAATA 974

5 AAGCTGAGCT ACGATTCCGA AAAAAAAA 1002

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

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Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

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Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

30

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
85 90 95

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Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
100 105 110

40

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
115 120 125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
130 135 140

45

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
145 150 155 160

Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser

	165		170		175
	Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln				
	180		185		190
5	Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro				
	195		200		205
	His Ile				
10	210				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 755 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

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(A) NAME/KEY: CDS

(B) LOCATION: 53..595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35	TCCTCGTGGG CCCTGACCTT CTCTCTGAGA GCCGGGCAGA GGCTCCGGAG CC ATG	55
		Met
		1
40	CAG GCC GAA GGC CAG GGC ACA GGG GGT TCG ACG GGC GAT GCT GAT GGC	103
	Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
45	CCA GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	151
	Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
	CCA GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGC	199
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	

	35	40	45	
	GCA GCA AGG GCC TCG GGC CCG AGA GGA GGC GCC CCG CGG GGT CCG CAT			247
	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His			
5	50	55	60	65
	GGC GGT GCC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG GCC AGG			295
	Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg			
		70	75	80
10	AGG CCG GAC AGC CGC CTG CTT CAG TTG CAC ATC ACG ATG CCT TTC TCG			343
	Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser			
		85	90	95
15	TCG CCC ATG GAA GCG GAG CTG GTC CGC AGG ATC CTG TCC CGG GAT GCC			391
	Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala			
	100	105	110	
	GCA CCT CTC CCC CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TCC			439
20	Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser			
	115	120	125	
	GGC AAC CTA CTG TTT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG			487
	Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu			
25	130	135	140	145
	CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG			535
	Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp			
		150	155	160
30	ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG			583
	Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly			
	165	170	175	
35	CAG AGG CGC TAAGCCCAGC CTGGCGCCCC TTCCTAGGTC ATGCCTCCTC			632
	Gln Arg Arg			
	180			
	CCCTAGGGAA TGGTCCCAGC ACGAGTGGCC AGTTCATTGT GGGGGCCTGA TTGTTTGTCTG			692
40	CTGGAGGAGG ACGGCTTACA TGTTTGTTC TGTAGAAAAT AAAGCTGAGC TACGAAAAAA			752
	AAA			755
45	(2) INFORMATION FOR SEQ ID NO:7:			

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
15 35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
20 65 70 75 80

Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
25 100 105 110

Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
30 115 120 125

Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
35 145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
165 170 175

Gly Gln Arg Arg
180

40

(2) INFORMATION FOR SEQ ID NO:8:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

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(B) LOCATION: 51..593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

20	CTCGTGGGCC CTGACCTTCT CTCTGAGAGC CGGGCAGAGG CTCGGAGCC ATG CAG	56
	Met Gln	
	1	
25	GCC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT GAT GGC CCA	104
	Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly Pro	
	5 10 15	
30	GGA GGC CCT GGC ATT CCT GAT GGC CCA GGG GGC AAT GCT GGC GGC CCA	152
	Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly Pro	
	20 25 30	
35	GGA GAG GCG GGT GCC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGG GCA	200
	Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly Ala	
	35 40 45 50	
40	GCA AGG GCC TCG GGG CCG GGA GGA GGC GCC CCG CGG GGT CCG CAT GGC	248
	Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro His Gly	
	55 60 65	
45	GGC GCG GCT TCA GGG CTG AAT GGA TGC TGC AGA TGC GGG GCC AGG GGG	296
	Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg Gly	
	70 75 80	
50	CCG GAG AGC CGC CTG CTT GAG TTC TAC CTC GCC ATG CCT TTC GCG ACA	344
	Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala Thr	
	85 90 95	
55	CCC ATG GAA GCA GAG CTG GCC CGC AGG AGC CTG GCC CAG GAT GCC CCA	392
	Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala Pro	

	100	105	110	
	CCG CTT CCC GTG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TCC GGC			440
	Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser Gly			
5	115	120	125	130
	AAC ATA CTG ACT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG CAG			488
	Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu Gln			
		135	140	145
10	CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG ATC			536
	Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp Ile			
		150	155	160
15	ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG CAG			584
	Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly Gln			
		165	170	175
	AGG CGC TAAGCCCAGC CTGGCGCCCC TTCCTAGGTC ATGCCTCCTC CCCTAGGGAA			640
20	Arg Arg			
		180		
	TGGTCCCAGC ACGAGTGGCC AGTTCAATTGT GGGGGCCTGA TTGTTTGTCTG CTGGAGGAGG			700
25	ACGGCTTACA TGTTTGTTC TGTAGAAAAT AAAACTGAGC TACGAAAAAA AAAAA			755

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	Met	Gln	Ala	Glu	Gly	Arg	Gly	Thr	Gly	Gly	Ser	Thr	Gly	Asp	Ala	Asp
	1				5					10					15	
40	Gly	Pro	Gly	Gly	Pro	Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly
				20				25						30		
	Gly	Pro	Gly	Glu	Ala	Gly	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala
45			35					40					45			
	Gly	Ala	Ala	Arg	Ala	Ser	Gly	Pro	Gly	Gly	Gly	Ala	Pro	Arg	Gly	Pro
		50					55						60			

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
5 85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
100 105 110

10 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
130 135 140

15 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145 150 155 160

20 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
165 170 175

Gly Gln Arg Arg
180

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 nucleotides
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCATGCAGG CCGAAGGC

18

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 nucleotides
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGGCCACTC GTGCTGGGA

19

(2) INFORMATION FOR SEQ ID NO:12:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGGATGGA AGGTGCCC

18

40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 nucleotides

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 CCCCACCGCT TCCCGTG

17

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

30

GGCTGAATGG ATGCTGCAGA

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